



Contents lists available at ScienceDirect

Developmental Biology

journal homepage: www.elsevier.com/developmentalbiology

Plenary Session II

Program/Abstract # 34**How a leaf is patterned**

Sarah Hake, Nathalie Bolduc, Devin O'Connor,
Jihyun Moon, Michael Lewis
USDA-ARS, UC Berkeley, Albany, CA, USA

The maize leaf is composed of two major tissues, a distal blade that tilts away from the stem and the more proximal sheath that tightly wraps around the stem. At the junction of the blade and sheath, the ligule and auricles are found. The auricles act as a hinge to let the blade lean back and the ligule is a flap of tissue, perhaps functioning as a gutter to prevent water from entering into the stem. Our goal is to understand how cells in a leaf primordia differentiate according to position and adopt specific cell types. We are using a number of maize mutants that affect the patterning in the leaf. *liguleless1*, *liguleless 2* and *Liguleless narrow* mutants remove the ligule and auricle. The *knotted1* family of homeobox genes displace the ligule and auricle when misexpressed in leaves. Using a combination of genomics, genetics and cell biology, we are studying the targets of KN1 and how KN1 interacts with auxin signaling. We are following the expression of *liguleless* genes and other markers during the early stages of patterning.

doi:[10.1016/j.ydbio.2011.05.049](https://doi.org/10.1016/j.ydbio.2011.05.049)

Program/Abstract # 35**A functional genomics investigation of neurogenesis**

François Guillemot
National Institute for Medical Research,
London, United Kingdom

We are interested in the developmental programmes that generate the extraordinary cell diversity of the mammalian brain from seemingly uniform progenitors. To gain access to such programmes, we have studied extensively the proneural transcription factors *Mash1/Ascl* and *Neurogenin2/Neurog2*. These factors promote neurogenesis and contribute to the specification of distinct neuronal populations throughout the embryonic nervous system and in discrete regions of the adult brain. We have begun to identify on a genome scale the transcriptional targets of proneural factors in different regions of the embryonic nervous system and in neural stem cell cultures. Our current results indicate that proneural proteins directly regulate large numbers of effector genes that are involved in all steps of neurogenesis. Functional analysis of these proneural targets is beginning to shed lights on the pathways that control important events in neural development, including the proliferation of neural progenitors and migration of new neurons, and how these pathways diverge in different brain regions.

doi:[10.1016/j.ydbio.2011.05.050](https://doi.org/10.1016/j.ydbio.2011.05.050)